

What is claimed is:

1. A method for detecting transition single-nucleotide polymorphisms at CpG sites in a target nucleic acid molecule, comprising:

- 5           a) providing a detectably labeled wild type or mutant target nucleic acid containing CpG sequences;
- b) contacting said wild type or mutant target nucleic acid with a homologous nucleic acid sequence isolated from a test subject, under conditions whereby
- 10       heteroduplexes form between said sequences;
- c) contacting said heteroduplex with MED1 protein, thereby forming a complex between the heteroduplex and MED1 and exposing said complex to hot alkali, said exposure resulting in cleavage of any
- 15       heteroduplexes containing a G:T mismatch on the T-containing strand; and
- d) detecting said cleavage product, if any.

2. A method as claimed in claim 1, wherein said

20       cleavage product is detected using a detection method selected from the group consisting of gel electrophoresis, capillary electrophoresis, and high performance liquid chromatography.

25       3. A method as claimed in claim 1, wherein said target nucleic acid contains a detectable label selected from the group of labels consisting of radioactive, fluorescent, chemiluminescent, and biotin.

30       4. A method for assessing the glycosylase activity of MED1 isolated from a patient sample, said method comprising:

- a) obtaining MED1 from a patient sample;
- b) contacting a first detectably labeled,
- 35       double-stranded oligonucleotide substrate containing a G:T

mismatch with MED1 isolated from a patient, thereby forming a first DNA/MED1 complex;

c) contacting a second detectably labeled, double-stranded oligonucleotide substrate containing a G:T mismatch with wild type MED1, thereby forming a second DNA/MED1 complex;

d) exposing said first and second complexes to alkali, said exposure causing cleavage of said oligonucleotide substrates at said G:T mismatch;

e) detecting said cleavage products, and

f) comparing the relative amounts of cleavage products obtained, a discrepancy in the amount of cleavage products obtained from said first and second complexes being indicative of altered MED1 glycosylase activity in the MED1 protein isolated from said patient.

5. A method as claimed in claim 4, wherein a nucleic acid sequence encoding said altered MED1 protein is isolated from said patient.

6. A method as claimed in claim 5, wherein said nucleic acid sequence encoding said altered MED1 protein is compared to a DNA sequence encoding wild type MED1, thereby identifying any alterations in said sequence isolated from said patient.

7. A method as claimed in claim 4, wherein said detectable label is selected from the group consisting of radioactive, fluorescent, chemiluminescent, and biotin.

8. A method as claimed in claim 4, wherein said cleavage products are detected via a method selected from the group consisting of gel electrophoresis, capillary electrophoresis, and high performance liquid chromatography.